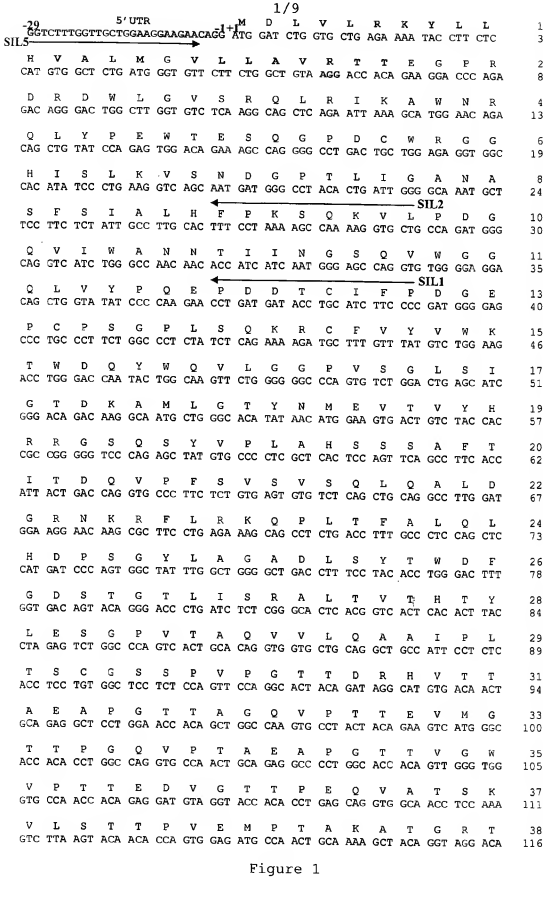
-29 5'UTR -1+1 M D L V L R K Y L L 10
GGTCTTTGGTTGCTGGAAGGAAGAACAGG ATG GAT CTG GTG CTG AGA AAA TAC CTT CTC 30
SIL5
H V A L M G V L L A V R T T E G P R 28
CAT GTG GCT CTG ATG GGT GTT CTT CTG GCT GTA AGG ACC ACA GAA GGA CCC AGA 84
D R D W L G V S R Q L R I K A W N R 46
GAC AGG GAC TGG CTT GGT GTC TCA AGG CAG CTC AGA ATT AAA GCA TGG AAC AGA 138
Q L Y P E W T E S Q G P D C W R G G 64
CAG CTG TAT CCA GAG TGG ACA GAA AGC CAG GGG CCT GAC TGC TGG AGA GGT GGC 192
H I S L K V S N D G P T L I G A N A 82
CAC ATA TCC CTG AAG GTC AGC AAT GAT GGG CCT ACA CTG ATT GGG GCA AAT GCT 246
SIL2
S F S I A L H F P K S Q K V L P D G 100
TCC TTC TCT ATT GCC TTG CAC TTT CCT AAA AGC CAA AAG GTG CTG CCA GAT GGG 300
Q V I W A N N T I I N G S Q V W G G 118
CAG GTC ATC TGG GCC AAC AAC ACC ATC ATC AAT GGG AGC CAG GTG TGG GGA GGA 354
SIL1
Q L V Y P Q E P D D T C I F P D G E 136
CAG CTG GTA TAT CCC CAA GAA CCT GAT GAT ACC TGC ATC TTC CCC GAT GGG GAG 408
P C P S G P L S Q K R C F V Y V W K 154
CCC TGC CCT TCT GGC CCT CTA TCT CAG AAA AGA TGC TTT GTT TAT GTC TGG AAG 462
T W D Q Y W Q V L G G P V S G L S I 172
ACC TGG GAC CAA TAC TGG CAA GTT CTG GGG GGC CCA GTG TCT GGA CTG AGC ATC 516
G T D K A M L G T Y N M E V T V Y H 190
GGG ACA GAC AAG GCA ATG CTG GGC ACA TAT AAC ATG GAA GTG ACT GTC TAC CAC 570
R R G S Q S Y V P L A H S S S A F T 208
CGC CGG GGG TCC CAG AGC TAT GTG CCC CTC GCT CAC TCC AGT TCA GCC TTC ACC 624
I T D Q V P F S V S V S Q L Q A L D 226
ATT ACT GAC CAG GTG CCC TTC TCT GTG AGT GTG TCT CAG CTG CAG GCC TTG GAT 678
G R N K R F L R K Q P L T F A L Q L 244
GGA AGG AAC AAG CGC TTC CTG AGA AAG CAG CCT CTG ACC TTT GCC CTC CAG CTC 732
H D P S G Y L A G A D L S Y T W D F 262
CAT GAT CCC AGT GGC TAT TTG GCT GGG GCT GAC CTT TCC TAC ACC TGG GAC TTT 786
G D S T G T L I S R A L T V T H T Y 280
GGT GAC AGT ACA GGG ACC CTG ATC TCT CGG GCA CTC ACG GTC ACT CAC ACT TAC 840
L E S G P V T A Q V V L Q A A I P L 298
CTA GAG TCT GGC CCA GTC ACT GCA CAG GTG GTG CTG CAG GCT GCC ATT CCT CTC 894
T S C G S S P V P G T T D R H V T T 316
ACC TCC TGT GGC TCC TCT CCA GTT CCA GGC ACT ACA GAT AGG CAT GTG ACA ACT 948
A E A P G T T A G Q V P T T E V M G 334
GCA GAG GCT CCT GGA ACC ACA GCT GGC CAA GTG CCT ACT ACA GAA GTC ATG GGC 1002
T T P G Q V P T A E A P G T T V G W 352
ACC ACA CCT GGC CAG GTG CCA ACT GCA GAG GCC CCT GGC ACC ACA GTT GGG TGG 1056
V P T T E D V G T T P E Q V A T S K 370
GTG CCA ACC ACA GAG GAT GTA GGT ACC ACA CCT GAG CAG GTG GCA ACC TCC AAA 1110
V L S T T P V E M P T A K A T G R T 388
GTC TTA AGT ACA ACA CCA GTG GAG ATG CCA ACT GCA AAA GCT ACA GGT AGG ACA 1164

Figure 1

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 P  E  V  S  T  T  E  P  S  G  T  T  V  T  Q  G  T  T    406
CCT GAA GTG TCA ACT ACA GAG CCC TCT GGA ACC ACA GTT ACA CAG GGA ACA ACT  1218

 P  E  L  V  E  T  T  A  G  E  V  S  T  P  E  P  A  G    424
CCA GAG CTG GTG GAG ACC ACA GCT GGA GAG GTG TCC ACT CCT GAG CCT GCG GGT  1272

 S  N  T  S  S  F  M  P  T  E  G  T  A  G  S  L  S  P    442
TCA AAT ACT AGC TCA TTC ATG CCT ACA GAA GGT ACT GCA GGC TCC CTG AGT CCC  1326

 L  P  D  D  T  A  T  L  V  L  E  K  R  Q  A  P  L  D    460
CTG CCG GAT GAC ACT GCC ACC TTA GTC CTG GAG AAG CGC CAA GCC CCC CTG GAT  1380

 C  V  L  Y  R  Y  G  S  F  S  L  T  L  D  I  V  Q  G    478
TGT GTT CTG TAT CGC TAT GGC TCC TTT TCC CTC ACC CTG GAC ATT GTC CAG GGT  1434

 I  E  S  A  E  I  L  Q  A  V  S  S  S  E  G  D  A  F    496
ATT GAG AGT GCT GAG ATC CTA CAG GCT GTG TCA TCC AGT GAA GGA GAT GCA TTT  1488

 E  L  T  V  S  C  Q  G  G  L  P  K  E  A  C  M  D  I    514
GAG CTG ACT GTG TCT TGC CAA GGC GGG CTA CCC AAG GAA GCC TGC ATG GAC ATC  1542

 S  S  P  G  C  Q  L  P  A  Q  R  L  C  Q  P  V  P  P    532
TCA TCG CCA GGG TGT CAG CTG CCT GCC CAG CGG CTG TGT CAG CCT GTG CCC CCC  1596

 S  P  A  C  Q  L  V  L  H  Q  V  L  K  G  G  S  G  T    550
AGC CCA GCC TGC CAG CTG GTT TTG CAC CAG GTA CTG AAG GGT GGC TCA GGG ACC  1650

 Y  C  L  N  V  S  L  A  D  A  N  S  L  A  M  V  S  T    568
TAC TGC CTC AAT GTG TCT TTG GCT GAT GCC AAT AGC CTG GCG ATG GTC AGC ACC  1704
SIL3 ──────────►

 Q  L  V  M  P  G  Q  E  A  G  L  R  Q  A  P  L  F  V    586
CAG CTT GTC ATG CCT GGG CAA GAA GCA GGC CTC AGG CAG GCT CCT CTG TTC GTG  1758

 G  I  L  L  V  L  T  A  L  L  L  A  S  L  I  Y  R  R    604
GGC ATC TTG CTG GTG CTA ACA GCT TTG TTG CTT GCA TCT CTG ATA TAC AGG CGA  1812

 R  L  M  K  Q  G  S  A  V  P  L  P  Q  L  P  H  G  R    622
AGA CTT ATG AAG CAA GGC TCA GCA GTC CCC CTT CCC CAG CTG CCA CAC GGT AGA  1866

 T  Q  W  L  R  L  P  W  V  F  R  S  C  P  I  G  E  S    640
ACC CAG TGG CTA CGT CTG CCC TGG GTC TTC CGC TCT TGC CCC ATT GGT GAG AGC  1920

 K  P  L  L  S  G  Q  Q  V  *  ◄──────────────────────SIL7  649
AAA CCC CTC CTC AGT GGA CAG CAG GTC TGA GTG CTC TTA TGT GAA GTC ATG ATT  1974
SIL4 ──────►

TAC CCA GGT GGA CAG CAA GGC CTG TCT TTT CTC TGG TCT TCC CTC AGA GAC TAC  2028
◄──────────────SIL6                                  (SEQ ID NO: 13)

CAT TGC CTG AAA TAA AGA CTC AGA ACT TG    Poly(A)  (SEQ ID NO: 12)      2057
◄──────────────SIL9
      3'UTR
```

Figure 1 (suite)

SIL10 →

GTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCCATGTGGCTCTGATGGGTGTTCTTCTGGC 80

TGTAAGGACCACAGAAGGTGAGTGTGGGATGTTGGACATGAACAAGTGTGAATTTGGGGTTGCACACCTGCTCTGTTTT 160

TCTCTCCCTAAAATGGAAGATATCAGTAGTGCTTCAGGTGTCTCCCACCCATTTGATTTAGTGAGGACATGGGCAACTGA 240

GCTCCCTCCCACATGAAGATTTGGGTGCATGTGTGTTCAGGCACTTGGGACTGAACCTGAAAACAACCCCATCTACCTG 320

← SIL8

GATGGGTGAGAGAACAGTATGTCTCCGTGGCCCTAATTTTGAGATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG 400

TAGTAAAATGAGTGGAAACTCATTTAGGCTTTGTCTCAGGCACTTGGGATAGGGTATTTAGGAGATAGAGAAAGATAGGA 480

GATAGGAGAAAGGAGAAAGAGGATGTGGTATTGGATAGAAGGGTAATGAGGCACCTCATCCCCTCTTTGGGATGGGCATG 560

GGTGAACACAGCCCAGGCTTTGTTCTGGGGCTGGAAGAGACAGGCAGAAGGGTCTCAGCTGAGCATCACATGAAAGGGC 640

TCTGGGGGATTGGGGCCTCGTGACAGGAGCAAGGCGGGTGGGGTGGGGATGGTGAGAGGGTCTGGAATGTCCCGTGCTGC 720

TCTGAGGAGGGAGGATTGGGAGTGGAGAAAGAATGGGGCATCTTATGATTCTCTTGTTCTTGTGGTGAGGTATTCAGTGG 800

GATAATTCTAGATCCTCCCCCAAGAGAATCAACCAGGTTTCTGGTACATGTTAGAGATGGAGTGAGGATAGTCTGTGATG 880

TGCAGAAATATCTACATTGTACCCCAGTGCCCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGGAACTTCTCCTTG 960

ATCTGACTTCCCTCATTCATGGTGTCATTTCAAGTCTTATTCTTTACTATGTTCGTTATTGTATTCTGGAAATATCCTG 1040

TTCATATGTGTCCACCCAAGGCTCTTAATATGTTGTCCTTACTTTTTGGATCCAGATTTTTAAAATCATAAGAAGACATT 1120

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CATATTAAGCAATGCCTTGGATTATAGTAATTTATGTATATGTCTATTTCATATACTTTAACCTGAACCCCTTCAGAACC 1920

ATTTCTTTTTCATTTCTTAAGTTCTTTGCACCTAGCCCAGTGCCTGGTACGTCGTGGGTATTCAGTAGATTAAAATGCAC 2000

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Figure 2

AAAAAAATTATAGTTCCCCAAATGGGGCACAGAAGACCCAGTGGACATAGAAGTTGGATAGACTTGGATTTAAACTGGTT 2960

ACCAGTATGTGACCCTGGACAAGTCACTGAATTGTTTGTTCTTCCATTCCCTTATCTATAGAATGGGGATGATAACACT 3040

TTAAAAGGTTCTTGTAAGGATTAAAATGTGATAATATAAAGATTTTAGCATAATGCCTGCCCTGTGCTGTGCTTAGTA 3120

CCTTAGTTTAGACGCTTTGCAACCCCATGGACTGTAGCCCACCAGGCTCCTCTGTCCATGTGGATTCTGCAGGCAAGAAT 3200

ACTGGAGTGGGTCACCATGCACTCCTCCAGGGGATCTTCCCAACTCAGGGATCGAACCCAGGTCCTAGCCTACAGTATTA 3280

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GTGTCCAGTGTAAGAATATACATGTGTGTGCTCAGTGGCTCAGTCGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC 3440

CGCGAAAGCTCCTCTGCCCATGGGATTGCCCAGCCAAGAATACTGGAGCAGGTTGCCATTTCTTCCTCCAGGGGATCTTT 3520

CAACACAGGGATTCAATCCTTGTCTCCTGTGTTTCCTGCATTGGCAGGTGTATTCTTTACCACTGAGCCACCTGGGAAAC 3600

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ATGATACCTGCATCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTTATGTCTGG 3920

AAGACCTGGGGTAAGAGTTTCCCTTCTCTGGCCTGTCATTCACACTTAAATTCACTTCTTCCTACCTGATCCCCTTTCTT 4000

TTGGTCTCATCCTTAAATTCTGTGAGTTTCCCTAATCTTCACTTCCCCCATGACTCCTTCCTCTTCCACAGCACCTAGTC 4080

AACTCTATTATACTTCTTTCTGGGAGCCCTGCTCCAATTATAGTCCCATCCATGGACCCTCTCATAAGGACTTTTTTCC 4160

TGCCCAACATATGCAAGCTTAAACTCTCTGAAATAACCATCCTTGATACATCTCCTGACCTTCCTTCTCTGGTTCCATCT 4240

CTAACCCTGCCCCAGTCTCCTTTGACCAGTAACCCCCTTCCCTACTCTTCTTTCCAAAAACCTCAGACCAATACTGGCAA 4320

GTTCTGGGGGGCCCAGTGTCTGGACTGAGCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGT 4400

CTACCACCGCCGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTGGTAAGGACTGAG 4480

GAGGGGACAAGGCCAGTTGCAGGGCAGGAGAAGGTGGGGAGGCTGGGCTGGACAGGAAAGGGAAAGAGGAAATGGTGTG 4560

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GTGGTGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCCCATTCCAGGCACTACAGATAGGCATGTGACAAC 5040

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CAGAGGCCCCTGGCACCACAGTTGGGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCC 5200

AAAGTCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAGTGTCAACTACAGAGCC 5280

CTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGGAGACCACACCTGGAGAGGTGTCCACTCCTGAGCCTG 5360

CGGGTTCAAATACTAGCTCATTCATGCCTACAGAAGGTACTGCAGGTAAGGGGCCACCATGAATGAGTTCATAGAGGTG 5440

GGGCATTTGTCACAGCTCTGAAGACCTGAAAGAATTGCTCAGGACCCAGATGTTACTCAATCCTTAGCTTAGCAGTGGAG 5520

TCCCCTCAGAATCTTCACTGGTTTTAAAACCCCCTAAGTCCCTCTTAATGGCACAGAATAGATCCAGAGTTCAGGAAACC 5600

AGGGTCTTCTCCTAGGCCAGGGGTAGAGAGCTTATTCTCTTCCTGAAGAGAAGTTCAGGAAGCAGTGTGTGATCATTT 5680

GGTGGTGGTGCTCAGTCATGTCTGACTCTTTGTGACCTCATGGACTATGGCCCACCAGGCTCCTCTGTCCATAGAATTCT 5760

Figure 2 (suite 1)

CCAGGCAAGAACACTGGAGTGGGTGGCCATTTCCTTCTCCAGGGGATTTTCCCTGCCCAGGGATTAAACCCGAATTGGCA 5840

GGTGGATTCTTTACCCGAGCCACCTAGAAAGTCCCATGTGATCATTAGATAATACTTATACCTCATTTTCTGATTAAGTG 5920

TAAACACAGAAATCTTTCTGACACCACTTCCCACCCCTGGATTCCCATCCCAAAGTAGGTTTACCTGGAATTGTGGTAGG 6000

AATACTAAAAAGGGAGAAGTGAGATAGTGACACTATGACTTAACACATGTCAAATGTCTGACCCAGGACCTGGCACAGTG 6080

TAGGGTGTGATAAACATTTGGGATGTCTAAAATTCTGACTCTAACCCTGTGACTCTGGGGCAGTCATTTCTCTTGGGCCT 6160

TTCTTTATCTTAAAAAATGAGAGTTTCCAGCTCTTGTCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA 6240

AAATGCTTGTTGGGCCTGTTTTCAGGTTAGTCATTTGCTTTTTGACTTTGCCTCTTTAATCCTCTCCTCCAGGCTCCCTG 6320

AGTCCCCTGCCGGATGACACTGCCACCTTAGTCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGG 6400

CTCCTTTTCCCTCACCCTGGACATTGTCCGTGAGTCTTGCCTACATTGTCCGTAAGCTGGTGGAGGAGGCGTGTGCTGC 6480

TTAGGGTTGCCCAGTGGAAGCACACCTTGGAAGGAATTACTCACCTGGACAAGGAGAATACCCAGATCCCAGGGGTTTCA 6560

TATGAAGGCAGAATGGGATTAGGGAGGCAGCCCGAGGACCTTCCTGGCCATGGGCCTTGGGGGAGGATAAGTAGAGGAGT 6640

CTCAGACTTAAAAAAATCTTGCAACTTTGCAGAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCAGTGAAG 6720

GAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGTGAGTGTCCCACGGTTGCCCTGAGAACTCCTGGGGTGACTGC 6800

TGTCCTGTTCTCTGGTGTCTAGTGTCCCTTCCCAGATTCCCTGACGTAAGCTGACATCTCTCCCAGGCTACCCAAGGAAG 6880

CCTGCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGCCCCCCAGCCCAGCCTGC 6960

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CATCCTGCTCCCACTCCTTTACCCCTTATTACCACCACCACTCTTCCTCATGGGAAGAAGAAACCACCAACCCCTTTGGG 7360

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CAGTGGAGAAGAACTCAGTGAACTGAGTTCTCCACCTGCCAGAAAGGCAAATCCCTAGGCCTGGAGGGCTGAGGTCCTCA 7680

AAGCAGGGAAGCCTGTAGGGTGAGAGGGAAATGGTCAGAGCTTACCATAAACATAAGAGAGGATAAACCCTGTTGGTGAG 7760

TGCCATTGACCACCACTAACCAGTATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC 7920

CCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGGTCTTCCGCTCTTGCCCCATTGGTGAGAG 8000

CAAACCCCTCCTCAGTGGACAGCAGGTCTGAGTGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGT 8080

CTTTTCTCTGGTCTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG SIL9 (SEQ ID NO: 14) 8138

Figure 2 (suite 2)

```
cDNA CH     GGTCTTTGGTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCC 60
cDNA RPE1   ------------------------------------------------------------

cDNA CH     ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGGACCACAGAAGGACCCAGAGACAGGG 120
cDNA RPE1   ------------------------------------------------------------

cDNA CH     ACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAG 180
cDNA RPE1   ------------------------------------------------------------

cDNA CH     AGTGGACAGAAAGCCAGGGGCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA 240
cDNA RPE1   ------------------------------------------------------------

cDNA CH     GCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTCTATTGCCTTGCACTTTC 300
cDNA RPE1   ------------------------------------------------------------

cDNA CH     CTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCA 360
cDNA RPE1   ------------------------------------------------------------

cDNA CH     ATGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTGATGATACCTGCA 420
cDNA RPE1   ------------------------------------------------------------

cDNA CH     TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTT 480
cDNA RPE1   ------------------------------------------------------------

cDNA CH     ATGTCTGGAAGACCTGGGACCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA 540
cDNA RPE1   -------------------CCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA  41
                               ************************************

cDNA CH     GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 600
cDNA RPE1   GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 101
            ************************************************************

cDNA CH     GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 660
cDNA RPE1   GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 161
            ************************************************************

cDNA CH     ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 720
cDNA RPE1   ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 221
            ************************************************************

cDNA CH     GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 780
cDNA RPE1   GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 281
            ************************************************************

cDNA CH     TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 840
cDNA RPE1   TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 341
            ************************************************************

cDNA CH     CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 900
cDNA RPE1   CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 401
            ************************************************************

cDNA CH     TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 960
cDNA RPE1   TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 461
            ************************************************************
```

Figure 3

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cDNA CH      ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG 1020
cDNA RPE1    ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG  521
             ************************************************************

cDNA CH      AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG 1080
cDNA RPE1    AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG  581
             ************************************************************

cDNA CH      GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG 1140
cDNA RPE1    GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG  641
             ************************************************************

cDNA CH      TCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG 1200
cDNA RPE1    TCTTAAGTACCACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG  701
             ********** ***************************************************

cDNA CH      TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG 1260
cDNA RPE1    TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG  761
             ************************************************************

cDNA CH      AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA 1320
cDNA RPE1    AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA  821
             ************************************************************

cDNA CH      TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG 1380
cDNA RPE1    TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG  881
             ************************************************************

cDNA CH      TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC 1440
cDNA RPE1    TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC  941
             ************************************************************

cDNA CH      TCACCCTGGACATTGTCCAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA 1500
cDNA RPE1    TCACCCTGGACATTGTC---AGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA  998
             ***************   ************************************

cDNA CH       GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1560
cDNA RPE1     GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1058
              ************************************************************

cDNA CH      GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1620
cDNA RPE1    GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1118
             ************************************************************

cDNA CH      CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1680
cDNA RPE1    CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1178
             ************************************************************

cDNA CH      ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1740
cDNA RPE1    ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1238
             ************************************************************

cDNA CH      TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1800
cDNA RPE1    TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1298
             ************************************************************

cDNA CH      TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1860
cDNA RPE1    TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1358
             ************************************************************

cDNA CH      CAGCAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1920
cDNA RPE1    CAGAAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1418
             *** ********************************************************
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Figure 3 (suite 1)

```
cDNA CH      TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1980
cDNA RPE1    TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1478
             ************************************************************

cDNA CH      TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1    TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
             ************************************************************

cDNA CH      CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 2086  (SEQ ID NO: 15)
cDNA RPE1    CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 1584  (SEQ ID NO: 16)
             ********************************************
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Figure 3 (suite 2)

```
Prot. CH        MDLVLRKYLLHVALMGVLLAVRTTEGPRDRDWLGVSRQLRIKAWNRQLYPEWTESQGPDC 60
Prot.RPE1       ------------------------------------------------------------

Prot.CH         WRGGHISLKVSNDGPTLIGANASFSIALHFPKSQKVLPDGQVIWANNTIINGSQVWGGQL 120
Prot.RPE1       ------------------------------------------------------------

Prot.CH         VYPQEPDDTCIFPDGEPCPSGPLSQKRCFVYVWKTWDQYWQVLGGPVSGLSIGTDKAMLG 180
Prot.RPE1       -------------------------------------QYWQVLGGPVSGLSIGTDKAMLG 23
                                                     **********************

Prot.CH         TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 240
Prot.RPE1       TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 83
                ************************************************************

Prot.CH         ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 300
Prot.RPE1       ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 143
                ************************************************************

Prot.CH         CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 360
Prot.RPE1       CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 203
                ************************************************************

Prot.CH         TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 420
Prot.RPE1       TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 263
                ************************************************************

Prot.CH         EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIVQGIE 480
Prot.RPE1       EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIV-SIE 322
                ************************************************. **

Prot.CH         SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 540
Prot.RPE1       SAEILQAVSSSEGDAFELTVSCQGGIPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 382
                ************************************************************

Prot.CH         HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 600
Prot.RPE1       HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 442
                ************************************************************

Prot.CH         IYRRRLMKQGSAVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 649  (SEQ ID NO: 17)
Prot.RPE1       IYRRRLMKQGSEVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 491  (SEQ ID NO: 18)
                *********** ************************************
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Figure 4